E+ 12	NT p16F- 207 1
GA GAA CAG	AATTCGGCACGAGCATGGAGCCTTCGGCTGACTGGCC
	ACGCCGCGCCCGGGTCGGGTAGAGGAGGTGCGGCGCTGCTG
•	NT ?16.3
	GAGGCGGTGCCCCAACGCACCGAATAGTTACGGTCGGAG
	GCCGATCCAGGTCATGGATGATGGCGCAGCGCCCCGAGTGGCGGAG
	CTGCTGCTCCACGGCGCGGGGGCCCAACTGCGCCGACCCCGCCA
	CTCTCACCCGACCCGTGCACCACGCTGCCCGGGAGGGCTTCTGGAC
	NT 716.5 ACCORGAGE GEORGE GORGE GEORGE GEORG
	ACGCIGGIGGIGCIGCACCOGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
	GATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGC
u M E	CATCGCGATGTCGCACGGTACCTGCGCGCGCGCTGCGGGGGGCACC
Table 1	(15 - 3(3)
	AGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGTCCCTC
	AGACATCCCCGATTGAAAGAACCAGAGAGGCTCTGAGAAACCTC
	L ETS
	GGGAAACTTAGATCATCAGTCACCGAAGGTCCTACAGGCCCACA
	ACTGCCCCCCCACACCCACCCCGCTTTCGTAGTTTTCATTTAGA
	AAATAGAGCTTTTAAAAATGTCCTGCCTTTTAACGTAGATATAA
	GCCTTCCCCCACTACCGTAAATGTCCATTTATATCATTTTTTATAT

Figure 1A

Figure 1B

## Figure 2A

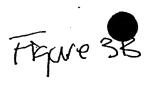
p16EX1	<	GGNGGNAAGNTGTGGGGAAAGTTTGGGGATGGAANACCAANCCCTCCTTTCNTTACCAA	60
		++	
p16EX1	<	${\tt ACNCTGGCTCTGNCGAGGCTNCNTCCGANTGGTNCCCCCGGGGGAGACCCAACCTGGGNC}$	120
016EX1 016EX13	< <	GACTTCAGGGNTGCNACATTCACTAAGTGCTNGGAGNTAATANCACCTCCTCCGAGCAN× TCNCTTATTGNTAGGANATAATAACACCtCCACcGAtAACT	180 41
		+++++++	
p16EX1 p16EX13	< <	TCGCTCACAGCGTCCCCTTACCTNGANAGATACCNCGxGxTCCCTCCAGAGGATTTGAGG TCaCTTACAACGTCCCNNTtCCTGgaAAGATACacaGCGTTCCCTCCAGAGGATTTGTGG	240 101
		+	
p16EX1 p16EX13	< <	GACAGGNTCGGAGGGGCTCTTCCCCCANCACCGGAGGAAGAAAGAGAGGGGGCTGACTGGACAGGGTNGGAGNGGTCTCTTCCNCCACCACCGGAGGAAGAAAGAGAGGGGGCTGNCTG	300 161
		ExiA (12)	
p165X1 p165X13	< <	GTCACCAGAGGGTGGGACGGACCGCGTGCGCTCGGCGNCTNCGGAGAGGGGGAGAACAGA TTCACCAGAGGGTGGGACGGACCNCGTACGCTCGNCGNCTNCGGAGAGGGGGAGAGCAGT	360 221
25 2000-2		I	
p1 <b>6E</b> X1 p1 <b>6E</b> X13	< <	CAACGGGCGGCGGGAGCAGCATGGATCCGGCGGCGGGGAGCAGCATGGANCCTTCGACT CANCGGNCGNCGGGGGAGCAACATGGAACCGNCGGCGGGGAGCAGCATGGANCCTTCGGCT	420 281
		,,,,,,,,	
P16NT2 7		GACNNNCTCCGGCCGGNGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAG GACTGACTGCCTCGC	49 435
p16EX13	<	GACTGCCTCGCCACGNCCCCGGGGTCGGGTAGAGGAGGTGCGGNCGCTNCTGGAG	341
		······································	
P16NT3	>	E ≠ 13 GT dTNANCCCGGGTA	15
P16NT2	_	GCGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAGGTxxGGGTA	109
p16EX13	<	GCGGGGNCTCTGNCCAACNCGCTAAAAN	369
		+++++++++	
P16NT3 P16NT2	> <	GAGGGTCTGCAGCGGAGCAGNGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG GAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG	75 169
		E71B	
P16NT3 P16NT2	> <	AATTGGAATCAGGTAGCGCTTCGANTCTCCGGAAAAAGGGGAGGCTTCCTGGGGAGTTNN AATTGGAATCAGGTAGCGCTTCGATTCTCCNGAAAAAGGGGAGGCTTCCTGGGGAGTTTT	135 229

		***************************************	
		CAGAAGGGGTTTGTAATCACAGNCCTCCNCCTGGCGACGCCCTGGGGGGGTTGGGAAGCCA CAGAAGGGGTTTGTAATCACAGACCTCCTCCTGGCGACGTCCTGGGGGGCTTGGGAAGCCA	
		+++	
		AGGAAGAGGAATGAGGAGNCACGCGCNTACAGNTCTCTCGAATNCTGANAAGATCTGAAGAGGAAGAGAGATNAGGAGCCACGCGCGTACAGATCTCTCGAATGCTGAGAAGATCTNAAG	
		++	
		GGGGGAACATATTTGTATTAGXATNNAAGTATGCTCTTTATCAGATACAAAATTCACGAA GGGGGAACATATTTGTATTAGCNTCCAAGTNTNCTCTNTATCANATACAAANT×C	315 404
		+++	
	>	CGTGTGGNATAAAAGGGAGTCTTAAAGAAATNTAAGATGTGCTGGGACTACTTAGCCTC	375
	>	CAANACACAGATNCCTGGATGGAGCT	401
T D T		······································	

POINT	>	AAAANNAAAAAAATCTCCCAGGCCTAACATAATTNTCAGGAAAGAAATTTCAGTAGTTG	60
6INT	>	NATCTCAGGGGAAATACAGGAAGTTAGCCTGGAGTAAAAGTCAGTC	120
.6INT	>	TGCTANATTGCCCGTGCCTCACAGTGCTCTCTGCCTGTGACGACAGCTCCNCAGAAGTTC	180
•		······································	
6INT	>	GGAGGATATAATGGAATTCATTGTGTACTGAAGAATGGATAGAGAACTCAAGAAGGAAAT	240
6INT 6EX±5	> <	TGGAAACTGGAAGCAAATGTAGGGGTAATTAGACACCTGGGGCTTGTGTGGGGGTCTGCT AANAAAAAAAATNgAtAANATagAGGAaT	300 31
		**************************************	
6INT 6EX15	> <	TGGCGGTGAGGGGGCTCTACACAAGCTTCCTTTCCGTCATGCCGNCCCCCACCCTGGCTC <u>GAACANATTAAAAtCAAAAAAACANAAGANAAGANAAGAAAAAAAAAAA</u>	360 91
		E* 184	
61 <b>NT</b> 6EX15		TGACCATTCTGTTCTCTGGCAGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTG NTAATGATAATTATAAAggTCAAGAGTCATTGATATMAAGGAAATCGAAGGGAAATCCTA	
		<u></u>	
SEXE		CTGCTGCTCCACGGCGCGGAGCCCAACTGCTCCGACGCCG	460
5EX14	>	CCTGCNACGACCCGCCACTCTCACCCGACCCGTG NCTCTCACGGTGGGAGGCCAACTGCGCCGAACCGCCACTCTCACCGACCCGCG	35
SEX15	-	acTagCACAANNGNATNAAAAANAATTcCCACGACCCCCCCCCCCCCCCCCCCCCCCCCCCCC	
		+	
EX2	>	CACGACGCTGTCCGGGAGGGTTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGGNG	95
EX14		CACGACGGTGCCCGGGAGGGGTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGCCG	116
EX15	<	CTCGACACTGCCCGGGAGGTCNTCCTGGACACGCTGGTGGTNCTCCACCGGNCCGGGGCA	271
EX2		CGGTTGGACGTGCGCGATGCCTGGGGCCGCCTNCCCGTGGxACCTGGTTGAGGAGCTGGG	
EX14		CGGCTGGACGTTCGNGATGCCTGGGGGCNTCTNTCCGTNGxACCTGGCTGAAGAGCTGGN	
EX15	<	CGTCTGGACGTGCCGATGCCTGGGNCCGNCTACCCGTGGTACCTGACTGAGGACCTGGG	331
		+++	
EX2		NCATCGCGATGTCGCACGGTACCTGCGCGCGCGTTGCGGGGGGCACCAGAGGXNAGTNACC	
EX14		NCATCGNGATGTCGCACGGCCNCTGTGTGNGGNTGCGGGGGGCACCATAGGTCAGTNTCC	
EX15	<	CCATCCCGATTTCGCNGGGTANCTGNGNGGGCTGNGGGGGGCCAANAGAGGxCANTACCC	391

## Figure 3A

916EX5	< xAAGTATGAGCGAAACNAATTGTGGTTTGAGAANAGGNAATCGTAGGGAACTTCGGGATC 6	0
	+	
⊃16EX5	< CCNCNGGGANCNCCAGAACCTGAGNCGCCNATTGGAAATNACAAACTGNCTGNATCACTC 1	20
>16EX5 >16EX9	CGNACCAGGTNCAAAAGATACCTGGGGANGCGGGAAGGGAA	
	+	
o16EX5 o16EX9	TTCGCNCCTXGGNATTGTGAGCAGCCTCTGAGACTCATTXATATNACACTCGTXTTTCTT 2     ATCGCGCCTTGGGANTGTGAGCNACCATTGAGACTCATNAATATAGCACTCGTTTTTCTT 6	
interes.	+++	
⊃16€x5 ⊃16€x9	< CTTACAACCCTGCGGNCCGCGCGCTCGCGCTTTCTCTGCCCTCCGCCGGGTGGACCTGGA 3 < CTTGCAACCCTGCGGNCCGCGCGCGCTCTCTCTCTCCCCCTCCGCNGGGTGGACCTGGA 1	
o16EX5 o16EX9	<pre>&lt; GCGCTTGAGCGGTCGCGCGCCTGGAGCAGCCAGGCGGNCAGTGGACTAGCTGCTGGACC 3 &lt; GCGCTTGAGCGGTCGGCGCNCCTGGANCAGCCAGGCGGCAGTGGACTACCTNCTGGACC 1</pre>	
i C	++++++++	
⊃16EX5 ⊃16EX9	< AGGGAGGTGTGGGAGAGCGGTGCGGCGGGTACATGCACGTGAAGCCATTGCGAGAACTT 4 < AGGGAGGTGTGGGAGAGCGGTGNCGGCGGGTACATGCACGTGAAGCCATTGCGAGAACTT 2	
)16EX5 )16EX9	<pre>&lt; TATCCATAAGTATTTCAATACCGGTAGGGACGCCAAGAGAGAG</pre>	
)16EX5 )16EX9	CATCTTTGACCTCAGGTTTCTAACGCCTGTTTTCTTTCTGCCCTCTGCAGACAACCCCGA 5 CATCTTTGACCTCAGGTTTCTAACGCCTGTTTTCTTTCTGCCCTCTGCAGACATCCCCGA 3	40 64
٠		
>16EX4	> AGAAATTAGATCATCAGTCACCGATG 2	
)16EX5 )16EX9	< TTGAAAGAACCAGAGAGGCTCTGAGAAACC < TTGAAAGAACCAGAGAGGGCTCTGAGAAACCTCCGGAAACTTAGxTCATCAxTCGCCGNAA 4:	70 24
)16EX4 )16EX9	> GTCCTACAGGGNCACAACTGNCCCCGCCACAACCCACCCCGNTTTCGTAGTTTTCATTTA 8 < AA	6 26
	± + + + + +	

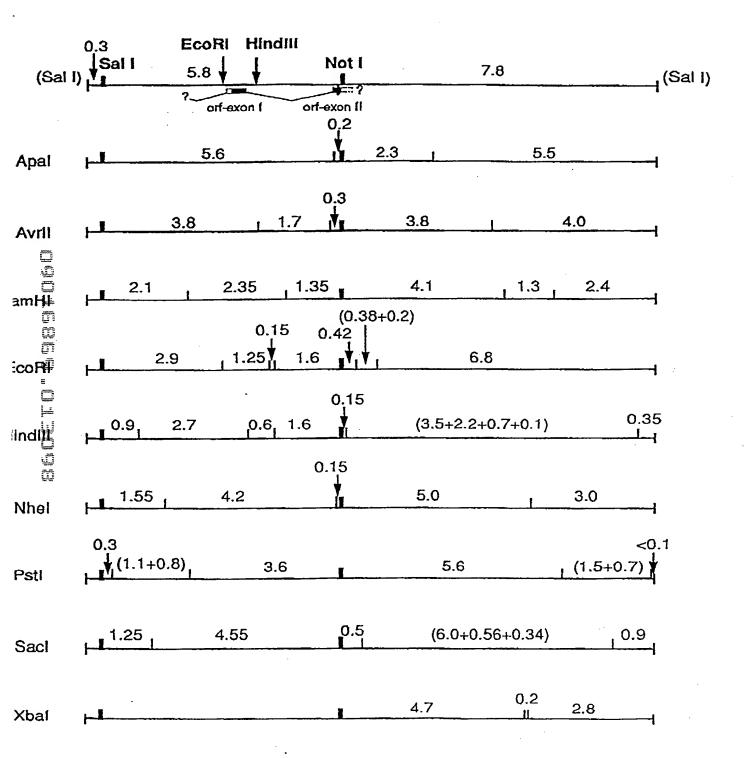


o16EX4	> GAAAATAGAGCTTTTAAAAATGTCCTGCCTTTTAACGTAGATATATGCCTTCCCCCACTA 14	6
	++	
p16EX4	> CCGNAAATGTCCATTTATATCATNTTTTATATATATATAAAAAATGTAAAAAAAGAAAAA 20	6
	++	
pl6EX4	> CACCGCTTCTGCCTTTTCACTGTGTTGGAGTTTTCTGGAGTGAGCACTCACGCCCTAAGC 26	6
	++	
p16EX6 p16EX6a p16EX4	> CANCNATNINCGGCATTICINGNGAGCCTCGTAGTCTCCGGATGNIGTCGACCTCGAG 58 > CANCNATNINCGGCATTICINGNGAGCCTCGTAGTCTCCGGATGNIGTCGACCTCGAG 58 > GCACATTCATGTGGGCATTCTTGCGAGCCTCGCAGNCTCCGGAAGCTGTCGACCTCGAG 32	}
p16EX6 p16EX6a p16 <u>E</u> X4	<ul> <li>&gt; GGGGGGNCCNGTACCCAATTCGNCCTATNGTGAGTCGTNTTACAATTCACTGGCCGCCGT 11</li> <li>&gt; GGGGGGNCCNGTACCCAATTCGNCCTATNGTGAGTCGTNTTACAATTCACTGGCCGCCGT 11</li> <li>&gt; GGGGGGNCCGGTACCCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGNCGNCGN 38</li> </ul>	.8
	+	
p1 62 X6 p1 62 X6a p1 62 X4	> TTTxACAACGTCGxTGxACTGGGAAAACCCTGGTGTTACCCAACTTxAATCGCCTTGNAG 17 > TTTxACAACGTCGxTGxACTGGGAAAACCCTGGTGTTACCCAACTTxAATCGCCTTGNAG 17 > TTTTACAACGTCGGTGGACTGGGAAAACCCCCGGNGTTACCCAACTTTAATCGNCTTGGAG 44	8
	++	
pleEX6 pleEX6a pleEX4	> NACATCCCCCTTTxCGCCAGCTGGTGTAATAGCGANGAGGCCCGCACCGATCGCCCTTCC 23 > NACATCCCCCTTTxCGCCAGCTGGTGTAATAGCGANGAGGCCCGCACCGATCGCCCTTCC 23 > GACATCCCCCTTTTCGCCAGNTGGGGTTATAGNGAAGAGGGCCNCACCNNTCGCCC 50	8
pleEX6 pleEX6a	<ul><li>CAACAGTTGNGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAAT 29</li><li>CAACAGTTGNGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAAT 29</li></ul>	-
	+++++++	
p16EX6 p16EX6a	> TCGCGTTANATCNTCGGTTAANTCAGCTCATNTTTTATCCAATAGGCCGANATCGGCANA 35 > TCGCGTTANATCNTCGGTTAANTCAGCTCATNTTTTATCCAATAGGCCGANATCGGCANA 35	8 8
	++	
p16EX6 p16EX6a	> ATCCCCAATAAATCAANAGAATAGACCGAGATAGGGTTGAGTGTCGTTCCAGTTNGGGAA 41 > ATCCCCAATAAATCAANAGAATAGACCGAGATAGGGTTGAGTGTCGTTCCAGTTNGGGAA 41	8 8
	++	
p16EX6 p16EX6a	> CANGAGTCCACTATTAAAGANCGTAGNCTCNAACGTCANAGGGCGAAAAACCNTNTTTCA 47 > CANGAGTCCACTATTAAAGANCGTAGNCTCNAACGTCANAGGGCGAAAAACCNTNTTTCA 47	8 8 .
	++	
p16EX6	> GNGGATTGGNCCACTACGCNTANCC 50	3.

Figure 4

cell	exon I	exon 2		cell	exon 1	exon 2
normal #1 normal #2	norm	norm		HTB173	norm	norm
normal #1	norm	norm		HTB172	norm	norm
A431	altered	absent		Tera2	norm	norm
SaOs2	altered	altered		GM130	norm	norm
HTB 125 SaOs2	absent	absent		00 ZRB75	norm	norm
MCF-7	absent	absent		HTB100	norm	norm
CCL119	absent	absent		HeLa	norm	norm
U18	absent	absent	·	CCL120	norm	norm
H9	absent	absent		WI38	norm	norm

## Figure 5



## Figure 6

Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Met Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp Pro \* p15: p13: p16:

Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg Thr Thr Phe Len Thr Leu Thr

Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg

Ala Ala Ala Gly Gly Thr .... Thr Ala Thr Gly Asp

Ser Ala \* Gly Cys Ser ....